REMARKS

The Sequence Listing submitted herewith includes the sequences identified in the claims, which were added by Applicant's amendment filed November 15, 2001. .

The undersigned hereby states that the computer readable form copy (CRF copy) of the Sequence Listing and the paper copy of the Sequence Listing, in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 03-1952** referencing docket no. 399632000623. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

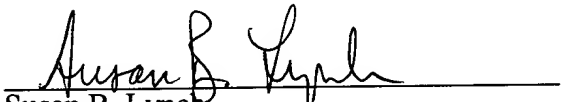
Dated: August 12, 2002 By: 

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EXHIBIT A

In the Claims:

146. (Amended) A method for making a peptide which comprises an HLA-A2.1 restricted T cell binding motif, said binding motif consisting of 9-10 amino acid residues, and wherein said peptide binds an HLA-A2.1 molecule, said method comprising the steps of

(e) providing an amino acid sequence of an antigen of interest;

(f) identifying within said sequence a subsequence consisting of 9-10 amino acid residues which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of L, M, I, V, A and T and a second amino acid anchor residue at the C-terminus of said subsequence selected from the group consisting of A and M (SEQ ID NOS: 350-351); or

which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of I, V, A and T and a second amino acid anchor residue at the C-terminus of said subsequence selected from the group consisting of L, V, I, A and M (SEQ ID NOS 352-353);

(g) identifying a fragment of said antigen which contains a subsequence identified in step (b); and

(h) preparing a peptide which contains said fragment.

147. (Amended) The method of claim 146, wherein said subsequence consists of 9 amino acid residues and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P (SEQ ID NOS: 354-355), or

position 3 or 7 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H (SEQ ID NOS: 356-359), or

position 6 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 360-361).

148. (Amended) The method of claim 147, wherein

position 1, 3 or 5 of said subsequence is selected from the group consisting of Y, F and W (SEQ ID NOS: 362-381), or

position 4 of said subsequence is selected from the group consisting of S, T and C (SEQ ID NOS: 382-389), or

position 7 of said subsequence is A (SEQ ID NO: 390-395).

149. (Amended) The method of claim 146, wherein the subsequence consists of 10 amino acid residues, and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P (SEQ ID NOS: 396-397), or

position 3 of said subsequence is not an amino acid selected from the group consisting of D and E (SEQ ID NOS: 398-399), or

position 4 of said subsequence is not an amino acid selected from the group consisting of R, K, H and A (SEQ ID NOS: 400-401), or

position 5 of said subsequence is not P (SEQ ID NOS: 402-403), or

position 7 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 404-405), or

position 8 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H (SEQ ID NOS: 406-407), or

position 9 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 408-409).

150. (Amended) The method of claim 149, wherein

position 1 of said subsequence is selected from the group consisting of A, Y, F and W (SEQ ID NOS: 410-423), or

position 3 of said subsequence is selected from the group consisting of L, V, I and M (SEQ ID NOS: 424-435) , or

position 4 of said subsequence is G (SEQ ID NOS: 436-447), or

position 8 of said subsequence is selected from the group consisting of Y, F, W, L, V, I and M (SEQ ID NOS: 448-459).

154. (Amended) A method to design a peptide which consists of less than 15 amino acids and which peptide comprises a subsequence consisting of 9-10 amino acids which binds an HLA-A2.1 molecule which method comprises

(e) providing an amino acid sequence of an antigen of interest;

(f) identifying within said sequence an amino acid subsequence consisting of 9-10 amino acid residues which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of L, M, I, V, A and T and a second amino acid anchor at the C-terminus of said subsequence selected from the group consisting of A and M (SEQ ID NOS: 350-351); or

which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of I, V, A and T and a second amino acid anchor at the C-terminus of said subsequence selected from the group consisting of L, V, I, A and M (SEQ ID NOS: 352-353);

(g) identifying a fragment of said antigen which contains a subsequence identified in step (b); and

(h) designing a peptide which comprises said fragment.

156. (Amended) The method of claim 154, wherein said subsequence consists of 9 amino acid residues and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P (SEQ ID NOS: 354-355), or

position 3 or 7 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H (SEQ ID NOS: 356-359), or

position 6 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 360-361).

157. (Amended) The method of claim 156, wherein

position 1, 3 or 5 of said subsequence is selected from the group consisting of Y, F and W (SEQ ID NOS: 362-381), or

position 4 of said subsequence is selected from the group consisting of S, T and C (SEQ ID NOS: 382-389), or

position 7 of said subsequence is A (SEQ ID NOS: 390-395).

158. (Amended) The method of claim 154, wherein the subsequence consists of 10 amino acid residues, and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P (SEQ ID NOS: 396-397), or

position 3 of said subsequence is not an amino acid selected from the group consisting of D and E (SEQ ID NOS: 398-399), or

position 4 of said subsequence is not an amino acid selected from the group consisting of R, K, H and A (SEQ ID NOS: 400-401), or

position 5 of said subsequence is not P (SEQ ID NOS: 402-403), or

position 7 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 404-405), or

position 8 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H (SEQ ID NOS: 406-407), or

position 9 of said subsequence is not an amino acid selected from the group consisting of R, K and H (SEQ ID NOS: 408-409).

159. (Amended) The method of claim 158, wherein

position 1 of said subsequence is selected from the group consisting of A, Y, F and W (SEQ ID NOS: 410-423), or

position 3 of said subsequence is selected from the group consisting of L, V, I and M (SEQ ID NOS: 424-435), or

position 4 of said subsequence is G (SEQ ID NOS: 436-447), or

position 8 of said subsequence is selected from the group consisting of Y, F, W, L, V, I and M (SEQ ID NOS: 448-459).

160. (Amended) An isolated peptide of less than 15 amino acids and which comprises an HLA-A2.1 binding motif of 9-10 amino acids in length;

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is I, and a second amino acid anchor at the C-terminus of said motif which is V, I, A or M (SEQ ID NOS: 460-461); or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is V, and a second amino acid anchor at the C-terminus of said motif which is L, V, I or M (SEQ ID NOS: 462-463); or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is A, and a second amino acid anchor at the C-terminus of said motif which is L, V or M (SEQ ID NOS: 464-465); or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is T, and a second amino acid anchor at the C-terminus of said motif which is L, I or M (SEQ ID NOS: 466-467); or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is L, and a second amino acid anchor at the C-terminus of said motif which is M (SEQ ID NOS: 468-469); or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is M, and a second amino acid anchor at the C-terminus of said motif which is A or M (SEQ ID NOS: 470-471); and

wherein a peptide that consists of said binding motif elicits a CTL response when complexed with said HLA-A2.1 molecule.

161. (Amended) An isolated peptide of claim 160, wherein said peptide has the sequence KVAELVHFL (SEQ ID NO: 472).